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# Inputs needed are
# tp[i,j,k], fp[i,j,k], pos[i,j,k], neg[i,j,k] i.e. summaries from
the 2x2 tables for replication i, study j, the kth test for study j
# You may want to re-order the indexes to make it easier for data
input to the arrays.
# ntests[j] a vector with number of tests per study
# nreps[j,k] the number of replcations of the kth test of study j
# t[j,k] indicates the test number for the kth test of study j.
# NTests is the total number of tests
# N1 is the number of studies with 2x2 data (ie your type 1 and type
3 studies)
# N2 is the number of studies with sensitivity/specificity data
# sens.mean[i,j,k] is the estimated sensitivity in ith rep of the
k'th test in study j, and sens.prec[i,j,k] is it's precision.

Model{
#Loop over studies reporting 2x2 tables. i=rep no., k=test no. in
study j
for (j in 1:N1){
  for (k in 1:ntests[j]){
    for (i in 1:nreps[j,k]){
      tp[i,j,k]~dbin(pi1[i,j,k],pos[i,j,k])
#Likelihood
      fp[i,j,k]~dbin(pi2[i,j,k],neg[i,j,k])
      tphat[i,j,k]<-pi1[i,j,k]*pos[i,j,k]
#Fitted values
      fphat[i,j,k]<-pi2[i,j,k]*neg[i,j,k]
      dev.tp[i,j,k]<-(2*(tp[i,j,k]*(log(tp[i,j,k])-
log(tphat[i,j,k]))) #Deviance contibution tp
      + (pos[i,j,k]-tp[i,j,k])*(log(pos[i,j,k]-tp[i,j,k]) -
log(pos[i,j,k]-tphat[i,j,k]))))
      dev.fp[i,j,k]<-(2*(fp[i,j,k]*(log(fp[i,j,k])-
log(fphat[i,j,k]))) #Deviance contibution fp
      + (neg[i,j,k]-fp[i,j,k])*(log(neg[i,j,k]-fp[i,j,k]) -
log(neg[i,j,k]-fphat[i,j,k]))))
    }
    dev[j,k]<-sum(dev.tp[1:nreps[j,k],j,k]) +
sum(dev.fp[1:nreps[j,k],j,k])
  }
  sumdev[j]<-sum(dev[j,1:ntests[j]])
}
}

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totresdev<- sum(sumdev[])

#Loop over all studies
for (j in 1:(N1)){
  for (k in 1:ntests[j]){
    for (i in 1:nreps[j,k]){
      logit(pi1[i,j,k])<- beta[t[j,k]]*theta[i,j,k]
+alpha[i,j,k]/2      #Model for sensitivity
      logit(pi2[i,j,k])<- theta[i,j,k] - alpha[i,j,k]/2
                      #Model for (1-specificity)
      theta[i,j,k]~dnorm(q[j,k],p.reps[1])
#Between rep variability
      alpha[i,j,k]~dnorm(a[j,k],p.reps[2])
    }
    q[j,k]~dnorm(Q[t[j,k]],p.stud[1])      #Between
study variability
    a[j,k]~dnorm(A[t[j,k]],p.stud[2])
  }
}

#PRIORS
for (k in 1:NTests){      #Loop over tests
  Q[k]~dnorm(0,.0001)
  A[k]~dnorm(0,.0001)
  log(beta.true[k])<-l.beta.true
  beta[k]<- include.slope[k]*beta.true[k] + (1-include.slope[k])
}
l.beta.true~dnorm(0,.0001)

for (m in 1:2){
  p.stud[m]<-pow(sd.stud[m],-2)
  p.reps[m]<-pow(sd.reps[m],-2)
  sd.stud[m]~dunif(0,5)
  sd.reps[m]~dunif(0,5)

# Save the prior distributions
sd.stud.prior[m]~dunif(0,5)
sd.reps.prior[m]~dunif(0,5)
}

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# Posterior and posterior predictive distributions
for(k in 1:NTests){
  theta.pred[k]~dnorm(Q[k],p.stud[1])
  alpha.pred[k]~dnorm(A[k],p.stud[2])
  logit(sens.pred[k])<-
beta[k]*theta.pred[k]+0.5*alpha.pred[k]
  logit(fpr.pred[k])<-theta.pred[k]-0.5*alpha.pred[k]
  spec.pred[k]<- 1 - fpr.pred[k]

  logit(TPR[k])<- (beta[k]*Q[k]+A[k]/2)
  logit(FPR[k])<- (Q[k]-A[k]/2)
  sensitivity[k]<-TPR[k]
  specificity[k]<-1-FPR[k]

  # Diagnostic odds ratio
  dor[k]<-(sensitivity[k]*specificity[k])/((1-
sensitivity[k])*(1-specificity[k]))
  #DOR[k] <- exp(A[k])
}
}

```